



A. Kubelik

1638

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/271,584
 DATE: 10/03/2000
 TIME: 16:25:14

Input Set : A:\salt seq listing.txt
 Output Set: N:\CRF3\10032000\I271584.raw

4 <110> APPLICANT: BLUMWALD, Eduardo
 5 APSE, Maris
 6 SNEDDEN, Wayne
 7 AHARON, Gilad
 9 <120> TITLE OF INVENTION: GENETIC ENGINEERING SALT TOLERANCE IN CROP PLANTS
 11 <130> FILE REFERENCE: 1110/0039
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/271,584
 14 <141> CURRENT FILING DATE: 1999-03-18
 16 <150> PRIOR APPLICATION NUMBER: US 60/078,474
 17 <151> PRIOR FILING DATE: 1998-04-01
 19 <150> PRIOR APPLICATION NUMBER: US 60/116,111
 20 <151> PRIOR FILING DATE: 1999-01-15
 22 <160> NUMBER OF SEQ ID NOS: 37
 24 <170> SOFTWARE: PatentIn Ver. 2.1, Word 97

Does Not Comply
 Corrected Diskette Needed

see pp. 1, 2

ERRORED SEQUENCES

2247 <210> SEQ ID NO: 37
 2248 <211> LENGTH: 30
 2249 <212> TYPE: DNA
 2250 <213> ORGANISM: Synthetic
 2252 <220> FEATURE:
 2253 <223> OTHER INFORMATION: Page 55 - Primer
 2255 <400> SEQUENCE: 37
 2257 cgcgtcgaca tgggtggatgc tctagtgtgc
 E--> 2258 1
 E--> 2262 37/37

30

Extraneous material at end of file must
 be deleted. It is causing an invalid base
 count error.

09/271, 584

p. 2
RECEIVE

<210> 23
<211> 378
<212> DNA
<213> Oryza sativa

<220>
<223> Figure 8(c)

<400> 23

caagaagcta tacattggaa ggcattctac tgaccgtgag gttgccetta tgatgetcat 60
ggcttacctt tcatatatgc tggctgagtt gctagatttg agcggcattc tcaccgtatt 120
cttctgtggt attgtaatgt cacattacac ttggcataac gtcacagaga gttcaagagt 180
tacaacaaag cacgcatttg caactctgtc cttcattgct gagacttttc tcttctgtga 240
tgttgggatg gatgcattgg atattgaaaa atgggaattt nccagtgaca gacctg^{na}aa 300
atccatt^{ng}g gtaagctcaa ttttgctagg gattggttcc tgattggaag ngctgctttt 360
naattcccc tggtggtc 378

Missing mandatory <220> to <223>
features to explain "n's" in the
sequence. See # 10 on Error Summary
Sheet.

This error
is also
indicated in

sequences

24, 25, 26, 27,
and 28.

Please check
the listing and
correct.

VERIFICATION SUMMARY DATE: 10/03/2000
PATENT APPLICATION: US/09/271,584 TIME: 16:25:15

Input Set : A:\salt seq listing.txt
Output Set: N:\CRF3\10032000\I271584.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1698 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1698 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1698 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:1699 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1699 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
M:340 Repeated in SeqNo=23
L:1700 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1700 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1714 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1714 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1714 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
M:340 Repeated in SeqNo=24
L:1717 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1730 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1730 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1730 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1731 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1731 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:1735 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1735 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1758 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
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L:1758 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1775 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
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L:1775 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1794 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1794 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:1794 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:1795 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1795 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:1796 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1796 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:1797 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1797 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:2258 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:37
M:254 Repeated in SeqNo=37
L:2262 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:2262 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:31 SEQ:37